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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2010; month=1; day=15; hr=11; min=25; sec=5; ms=832;]

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Application No: 10596024

Version No: 2.0

Input Set:**Output Set:****Started:** 2009-12-29 16:23:06.670**Finished:** 2009-12-29 16:23:09.284**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 614 ms**Total Warnings:** 25**Total Errors:** 0**No. of SeqIDs Defined:** 35**Actual SeqID Count:** 35

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2009-12-29 16:23:06.670
Finished: 2009-12-29 16:23:09.284
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 614 ms
Total Warnings: 25
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No. of SeqIDs Defined: 35
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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (26)
W 402	Undefined organism found in <213> in SEQ ID (27)

SEQUENCE LISTING

<110> National Research Council of Canada

<120> FATTY ACID ELONGASE (FAE) GENES AND THEIR UTILITY IN INCREASING
ERUCIC ACID AND OTHER VERY LONG-CHAIN FATTY ACID PROPORTIONS IN SEED OIL

<130> PAT 989W-2

<140> 10596024

<141> 2009-12-29

<150> US 60/524,645

<151> 2003-11-25

<160> 35

<170> PatentIn version 3.5

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<211> 18

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<213> Artificial

<220>

<223> F1 Forward Primer

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<223> Coded by F1 Forward Primer

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<210> 3

<211> 18

<212> DNA

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<223> R1 Reverse Primer

<400> 3

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<223> R2 Reverse Primer

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<212> DNA

<213> Artificial

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<223> F3 Forward Primer

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<211> 30

<212> DNA

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<220>

<223> R3 Reverse Primer

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<223> R4 Reverse Primer

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<212> PRT
<213> Tropaeolum majus

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20 25 30

Ile Thr His Ala Met Tyr Leu Phe Leu Thr Pro Leu Leu Leu Ile Met
35 40 45

Ser Ala Gln Ile Ser Thr Phe Ser Ile Gln Asp Phe His His Leu Tyr
50 55 60

Asn His Leu Ile Leu His Asn Leu Ser Ser Leu Ile Leu Cys Ile Ala
65 70 75 80

Leu Leu Leu Phe Val Leu Thr Leu Tyr Phe Leu Thr Arg Pro Thr Pro
85 90 95

Val Tyr Leu Leu Asn Phe Ser Cys Tyr Lys Pro Asp Ala Ile His Lys
100 105 110

Cys Asp Arg Arg Arg Phe Met Asp Thr Ile Arg Gly Met Gly Thr Tyr
115 120 125

Thr Glu Glu Asn Ile Glu Phe Gln Arg Lys Val Leu Glu Arg Ser Gly
130 135 140

Ile Gly Glu Ser Ser Tyr Leu Pro Pro Thr Val Phe Lys Ile Pro Pro
145 150 155 160

Arg Val Tyr Asp Ala Glu Glu Arg Ala Glu Ala Glu Met Leu Met Phe
165 170 175

Gly Ala Val Asp Gly Leu Phe Glu Lys Ile Ser Val Lys Pro Asn Gln
180 185 190

Ile Gly Val Leu Val Val Asn Cys Gly Leu Phe Asn Pro Ile Pro Ser
195 200 205

Leu Ser Ser Met Ile Val Asn Arg Tyr Lys Met Arg Gly Asn Val Phe
210 215 220

Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Val Ile Ser Ile
225 230 235 240

Asp	Leu	Ala	Lys	Asp	Leu	Leu	Gln	Val	Arg	Pro	Asn	Ser	Tyr	Ala	Leu	245	250	255	
Val	Val	Ser	Leu	Glu	Cys	Ile	Ser	Lys	Asn	Leu	Tyr	Leu	Gly	Glu	Gln	260	265	270	
Arg	Ser	Met	Leu	Val	Ser	Asn	Cys	Leu	Phe	Arg	Met	Gly	Gly	Ala	Ala	275	280	285	
Ile	Leu	Leu	Ser	Asn	Lys	Met	Ser	Asp	Arg	Trp	Arg	Ser	Lys	Tyr	Arg	290	295	300	
Leu	Val	His	Thr	Val	Arg	Thr	His	Lys	Gly	Thr	Glu	Asp	Asn	Cys	Phe	305	310	315	320
Ser	Cys	Val	Thr	Arg	Lys	Glu	Asp	Ser	Asp	Gly	Lys	Ile	Gly	Ile	Ser	325	330	335	
Leu	Ser	Lys	Asn	Leu	Met	Ala	Val	Ala	Gly	Asp	Ala	Leu	Lys	Thr	Asn	340	345	350	
Ile	Thr	Thr	Leu	Gly	Pro	Leu	Val	Leu	Pro	Met	Ser	Glu	Gln	Leu	Leu	355	360	365	
Phe	Phe	Ala	Thr	Leu	Val	Gly	Lys	Lys	Val	Phe	Lys	Met	Lys	Leu	Gln	370	375	380	
Pro	Tyr	Ile	Pro	Asp	Phe	Lys	Leu	Ala	Phe	Glu	His	Phe	Cys	Ile	His	385	390	395	400
Ala	Gly	Gly	Arg	Ala	Val	Leu	Asp	Glu	Leu	Glu	Lys	Asn	Leu	Lys	Leu	405	410	415	
Ser	Ser	Trp	His	Met	Glu	Pro	Ser	Arg	Met	Ser	Leu	Tyr	Arg	Phe	Gly	420	425	430	
Asn	Thr	Ser	Ser	Ser	Ser	Leu	Trp	Tyr	Glu	Leu	Ala	Tyr	Ser	Glu	Ala	435	440	445	
Lys	Gly	Arg	Ile	Lys	Lys	Gly	Asp	Arg	Val	Trp	Gln	Ile	Ala	Phe	Gly	450	455	460	

Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala Leu Arg Asn Val
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Asn Pro Ala Glu Glu Lys Asn Pro Trp Met Asp Glu Ile His Leu Phe
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Pro Val Glu Val Pro Leu Asn
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<211> 1765
<212> DNA
<213> *Tropaeolum majus*

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tcactcatgc aatgtatctt tttctaacc cttcttcttct cataatgtct gctcaaactc 180
caactttctc tattcaagat tttcaccatc tttataacca tcttatcctc cacaatctct 240
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cgactgtgtt taaaattcct cctagggttt acgatgcgga ggaacgcgcg gaggctgaga 540
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ttgtgaatcg ctacaagatg agagggaatg tttttagtta taatttggtt ggaatgggtt 720
gtagtgccgg tgtgatttcg attgatcttg cttaaagatct tcttcagggt cgtcccaact 780
catatgcttt ggtggttagt ttggaatgta tctcgaagaa cttgtatctc ggtgaacaaa 840
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tcggatattt tttatcgaag aacctaatgg ctgttgccgg agacgcattg aagactaata 1080
tcacaaccct cggaccactt gttctacca tgtcgaaca attactcttc ttcgctactt 1140
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acacgtcgag tagttcgctt tggtagcagt tggcttattc ggaggcgaaa gggagaataa      1380
agaagggaga tcgagtatgg caaatcgcggt ttgggtcggg atttaagtgt aacagtgcgg      1440
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<210> 24
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<212> PRT
<213> Crambe abyssinica

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<400> 24

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Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
          20              25              30

```

```

Ala Ser Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
          35              40              45

```

```

Leu Gln His Asn Val Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
          50              55              60

```

```

Phe Gly Ser Ile Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu
65           70              75              80

```

```

Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr Gln Cys Arg Ser Ser Ile
          85              90              95

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Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Phe
          100             105             110

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Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
115 120 125

Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
130 135 140

Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
145 150 155 160

Thr Glu Gln Val Ile Val Gly Ala Leu Lys Asn Leu Phe Glu Asn Thr
165 170 175

Lys Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
180 185 190

Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
195 200 205

Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
210 215 220

Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225 230 235 240

Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn
245 250 255

Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
260 265 270

Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Arg Asp Arg
275 280 285

Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
290 295 300

Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305 310 315 320

Gly Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Glu Val Ala Gly
325 330 335

Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro

340

345

350

Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Ala Lys Lys Leu
 355 360 365

Phe Lys Asp Lys Val Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380

Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400

Leu Glu Lys Asn Leu Gly Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

Trp Val Ala Leu Ser Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Ala Lys
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Ser Glu Thr Arg Ala Gln Asn Gly Arg Ser
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<211> 1521

<212> DNA

<213> Crambe abyssinica

<400> 25

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cttcaccact tatattattc ctatctccaa cacaacgtca taaccatagc tccactcttt 180

gcctttaccg ttttcggttc gattctctac atcgtgaccc ggcccaaacc gggttacctc 240

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<211> 506

<212> PRT

<213> Arabidopsis sp.

<400> 26

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
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Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu